Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application. Please amend the claims as follows.

Claim 1 (currently amended): An isolated nucleic acid comprising nucleic acids selected from the group consisting of:

the sequence SEQ ID NO:1,

the genomic sequences of variant erythroviruses, called erythrovirus type V9, which, molecularly, cannot be recognized as an erythrovirus B19 because it exhibits a genetic divergence ≥ 10% over the whole genome with respect to the erythrovirus B19 sequences and which exhibit a genetic divergence of less than or equal to 6% with respect to the sequence SEQ ID NO:1, and

[the] erythrovirus genomic sequences ~~capable of hybridizing~~ which hybridize under stringent conditions with one of the following sequences: SEQ ID NO:45-80, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119 and SEQ ID NO:120.

Claim 2 (previously presented): The nucleic acid of Claim 1 wherein the nucleic acid exhibits a restriction profile according to Figures 7.1 to 7.3.

Claim 3 (currently amended): Fragments of the nucleic acids according to Claim 1~~, which are capable of allowing the detection of an erythrovirus V9, characterized in that they are~~ selected from the group consisting of:

a) the sequences SEQ ID NO:81, SEQ ID NO:83, SEQ. ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91 or SEQ ID NO:93,

b) the sequences SEQ ID NO: 2-80,

c) the sequences SEQ ID NO:105-121, and

d) the sequences complementary to the preceding sequences of parts 3a)-3c), wherein the fragments comprise at least 17 nucleotides derived from the preceding sequences or their complementary sequences.

Claim 4 (currently amended): [A] The fragment according to Claim 3, selected from the group consisting of the sequences SEQ ID NO:45-80, 108 and NO:110, their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and wherein the selected sequence serves ~~is capable of serving~~ as a probe in the specific identification of an erythrovirus V9 or of a related erythrovirus.

Claim 5 (currently amended): [A] The fragment according to Claim 3, selected from the group consisting of the sequences SEQ ID NO:2-80 and the sequences SEQ ID NO: 105-121, their complementary sequences, the sequences of at least 17 nucleotides derived from these sequences and the sequences comprising the said sequences and wherein the selected sequence ~~is capable of serving~~ serves as a primer for the amplification of sequences derived from an erythrovirus.

Claim 6 (currently amended): A pair of primers~~, characterized in that they are~~ selected from the group consisting of:

pair A: primers SEQ ID NO:111 and SEQ ID NO: 112

pair B: primers SEQ ID NO:105 and SEQ ID NO:106;

pair C: one of the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112 and one of the sequences SEQ ID NO:45-80, 108 or 110;

pair D: primer SEQ ID NO:107 and primer SEQ ID NO:109;

pair E: two primers selected from the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and

pair F: two primers selected from the sequences SEQ ID NO:45-80, 108 or 110.

Claim 7 (currently amended): A variant erythrovirus~~, characterized in that it~~ which cannot be recognized molecularly as an erythrovirus B19 genome~~, and~~ in that it exhibits a genetic divergence of less than or equal to 6% with the sequence SEQ ID NO:1 and in that its genome hybridizes specifically, under stringent conditions with one of the sequences SEQ ID NO:45 to 80, 108 and 110.

Claim 8 (currently amended): A plasmid~~, characterized in that it comprises~~ comprising the viral genome of a variant erythrovirus strain~~, called~~ erythrovirus V9, which cannot be recognized molecularly as an erythrovirus B19 and which exhibits with the latter a genetic divergence of $\geq$ 10% over the whole genome with respect to the erythrovirus B19 sequences and a genetic divergence of less than or equal to 6% with the sequence SEQ ID NO:1 or a fragment thereof, according to Claim 3.

Claim 9 (currently amended): A plasmid, according to Claim 8, ~~characterized in that it includes~~ comprising ~~the~~ sequence SEQ ID NO:1.

Claim 10 (currently amended): A diagnostic reagent for the differential detection of type V9 erythroviruses~~, characterized in that it is~~ selected from the sequences SEQ ID NO:45-80, 108 and 110, their complementary sequences, and the sequences of at least 17 nucleotides, derived from these sequences.

Claim 11 (currently amended): A method for the rapid and differential diagnosis of erythroviruses, by hybridization and/or gene amplification, using a biological sample as starting material, ~~which process is characterized in that it comprises~~ comprising:

(1) contacting ~~a step in which~~ a biological sample to be analyzed ~~is brought into contact~~ with at least one probe of sequence SEQ ID NO:45-80, 108 or 110, and

(2) detecting ~~a step in which~~ the product (s) resulting from the erythrovirus nucleotide sequence-probe interaction ~~is (are) detected~~ by any appropriate means.

Claim 12 (currently amended): The method according to Claim 11~~, characterized in that it comprises~~ comprising, prior to step (1):

~~a step of~~ extracting [of] the nucleic acid to be detected, belonging to the virus genome, which may be present in the biological sample, and

at least one gene amplification cycle.

Claim 13 (currently amended): The method according to Claim 12~~, characterized in that~~ wherein the amplification cycles are carried out with the ~~air~~ aid of a pair of primers selected from the group consisting of:

pair A: primers SEQ ID NO:111 and SEQ ID NO:112;

pair B: primers SEQ ID NO:105 and SEQ ID NO:106;

pair C: one of the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112 and one of the sequences SEQ ID NO:45-80, 108 or 110;

pair D: primer SEQ ID NO:107 and primer SEQ ID NO:109;

pair E: two primers selected from the sequences SEQ ID NO:2-44, 105, 106, 107, 109, 111 or 112; and

pair F: two primers selected from the sequences SEQ ID NO:45-80, 108 or 110.

Claim 14 (currently amended): A method for the rapid and differential diagnosis of erythroviruses~~, characterized in that it comprises~~ comprising:

~~a step of~~ extracting [of] the nucleic acid to be detected, belonging to the virus genome, which may be present in the biological sample,

at least one gene amplification cycle with the aid of a pair of primers according to Claim 6, and

~~the detection of~~ detecting the amplified product~~, on the one hand,~~ by hybridization with the sequence SEQ ID NO:121 ~~and, on the other hand,~~ by the action of the restriction enzyme MunI or both.

Claim 15 (canceled)

Claim 16 (currently amended): A method of screening and typing an erythrovirus V9 or a related virus~~, characterized in that it comprises~~ comprising bringing a probe selected from the group consisting of the sequences according to Claim 4, into contact with the nucleic acid of the virus to be typed, and detecting the nucleic acid-probe hybrid obtained.

Claim 17 (previously presented): A product of translation, characterized in that it is encoded by a nucleotide sequence according to Claim 1.

Claim 18 (previously presented): A protein, characterized in that it is capable of being expressed with the aid of a nucleotide sequence according to Claim 1.

Claim 19 (previously presented): A protein or peptide derived from a variant erythrovirus type V9, as defined in Claim 1 and selected from the sequences:

a) SEQ ID NO:82 (NS1 protein), SEQ ID NO:86 (VP1 protein), SEQ ID NO:88 (single VP1 protein), SEQ ID NO:92 (VP2 protein) and SEQ ID NO:95-104, namely fragments of the VP1 protein [VP1a peptide (SEQ ID NO:95); VP1b peptide (SEQ ID NO:96); VP1c peptide (SEQ ID NO:97); peptide VP1d (SEQ ID NO:98); peptide VP1e (SEQ ID NO:99); peptide VP1f (SEQ ID NO:100)], or fragments of the VP2 protein [peptide VP2a (SEQ ID NO:101); peptide VP2b (SEQ ID NO:102); peptide VP2c (SEQ ID NO:103); peptide VP2d (SEQ ID NO:104)], and

b) the sequences derived from sequences a) comprising between 7 and 50 amino acids.

Claim 20 (previously presented): An immunogenic composition comprising one or more products of translation of the nucleotide sequences according to Claim 17.

Claim 21 (previously presented): An antibody directed against one or more of the peptides or proteins according to Claim 17.

Claim 22-23 (canceled).

Claim 24 (previously presented): A method of *in vitro* screening diagnosis of infection of an individual with an erythrovirus comprising detecting hybridization of the individual's nucleic acid with a nucleic acid according to Claim 1.

Claim 25 (previously presented): The method of claim 24 comprising gene amplification.

Claim 26 (previously presented): The method of claim 16 wherein the probe is labeled.

Claim 27 (previously presented): The method of claim 16 wherein the nucleic acid of the virus to be typed is labeled.

Claim 28 (previously presented): An immunogenic composition comprising one or more of the proteins of claim 18.

Claim 29 (previously presented): An immunogenic composition comprising one or more of the peptides or proteins of claim 19.

Claim 30 (previously presented): An antibody directed against one or more of the proteins of claim 18.

Claim 31 (previously presented): An antibody directed against one or more of the proteins of claim 19.

Claim 32 (previously presented): A method for the immunological *in vitro* screening diagnosis of infection of an individual with an erythrovirus comprising detecting anti-erythrovirus V9 antibodies by contacting a biological sample with a peptide according to claim 17 and detecting the association of such a peptide with antibodies contained in the biological sample by an appropriate means.

Claim 33 (previously presented): The method of claim 32 wherein the appropriate detection means is selected from the group consisting of EIA, ELISA, RIA, and fluorescence.

Claim 34 (previously presented): A method for the immunological *in vitro* screening diagnosis of infection of an individual with an erythrovirus comprising detecting erythrovirus V9 viral proteins by contacting a biological sample with an antibody according to claim 21 and detecting the association of such an antibody with erythrovirus V9 viral proteins contained in the biological sample by an appropriate means.

Claim 35 (previously presented): The method of claim 34 wherein the appropriate detection means is selected from the group consisting of EIA, ELISA, RIA, and fluorescence.

Claim 36 (currently amended): An erythrovirus diagnostic kit comprising at least one probe of sequence SEQ ID NO: 45-80, 108 or 110, or a primer that hybridizes to a sequence of SEQ ID NO: 1 of claim 1 under stringent conditions ~~and/or a pair of primers selected from the group consisting of, and/or a peptide encoded by, or capable of being expressed with the aid of a nucleic acid of Claim 1, and/or an antibody directed against such peptides~~.

Claim 37 (previously presented): The diagnostic reagent of claim 10 wherein the reagent is labeled with an appropriate marker.

Claim 38 (previously presented): The nucleic acid of claim 1 comprising SEQ ID NO:1.